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TECH CENTER 1600/2900



1653

PHD

RAW SEQUENCE LISTING

DATE: 05/21/2002

PATENT APPLICATION: US/09/600,985

TIME: 13:33:12

Input Set : A:\568_1.txt

Output Set: N:\CRF3\05212002\I600985.raw

ENTERED

4 <110> APPLICANT: Madison, Edwin L
 6 <120> TITLE OF INVENTION: TISSUE TYPE PLASMINOGEN ACTIVATOR (t-PA)
 7 VARIANTS HAVING ZYMOGEN CHARACTERISTICS: COMPOSITIONS AND
 8 METHODS OF USE
 10 <130> FILE REFERENCE: TSRI 568.1
 12 <140> CURRENT APPLICATION NUMBER: US 09/600,985
 13 <141> CURRENT FILING DATE: 2000-11-13
 15 <150> PRIOR APPLICATION NUMBER: PCT/WO98/21320
 16 <151> PRIOR FILING DATE: 1996-11-12
 18 <160> NUMBER OF SEQ ID NOS: 10
 20 <170> SOFTWARE: FastSEQ for Windows Version 4.0
 22 <210> SEQ ID NO: 1
 23 <211> LENGTH: 527
 24 <212> TYPE: PRT
 25 <213> ORGANISM: Homo sapiens
 27 <400> SEQUENCE: 1
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 30 Gln His Gln Ser Trp Leu Arg Pro Val Leu Arg Ser Asn Arg Val Glu
 31 20 25 30
 32 Tyr Cys Trp Cys Asn Ser Gly Arg Ala Gln Cys His Ser Val Pro Val
 33 35 40 45
 34 Lys Ser Cys Ser Glu Pro Arg Cys Phe Asn Gly Gly Thr Cys Gln Gln
 35 50 55 60
 36 Ala Leu Tyr Phe Ser Asp Phe Val Cys Gln Cys Pro Glu Gly Phe Ala
 37 65 70 75 80
 38 Gly Lys Cys Cys Glu Ile Asp Thr Arg Ala Thr Cys Tyr Glu Asp Gln
 39 85 90 95
 40 Gly Ile Ser Tyr Arg Gly Thr Trp Ser Thr Ala Glu Ser Gly Ala Glu
 41 100 105 110
 42 Cys Thr Asn Trp Asn Ser Ser Ala Leu Ala Gln Lys Pro Tyr Ser Gly
 43 115 120 125
 44 Arg Arg Pro Asp Ala Ile Arg Leu Gly Leu Gly Asn His Asn Tyr Cys
 45 130 135 140
 46 Arg Asn Pro Asp Arg Asp Ser Lys Pro Trp Cys Tyr Val Phe Lys Ala
 47 145 150 155 160
 48 Gly Lys Tyr Ser Ser Glu Phe Cys Ser Thr Pro Ala Cys Ser Glu Gly
 49 165 170 175
 50 Asn Ser Asp Cys Tyr Phe Gly Asn Gly Ser Ala Tyr Arg Gly Thr His
 51 180 185 190
 52 Ser Leu Thr Glu Ser Gly Ala Ser Cys Leu Pro Trp Asn Ser Met Ile
 53 195 200 205
 54 Leu Ile Gly Lys Val Tyr Thr Ala Gln Asn Pro Ser Ala Gln Ala Leu

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55      210      215      220
56 Gly Leu Gly Lys His Asn Tyr Cys Arg Asn Pro Asp Gly Asp Ala Lys
57 225      230      235      240
58 Pro Trp Cys His Val Leu Lys Asn Arg Arg Leu Thr Trp Glu Tyr Cys
59      245      250      255
60 Asp Val Pro Ser Cys Ser Thr Cys Gly Leu Arg Gln Tyr Ser Gln Pro
61      260      265      270
62 Gln Phe Glu Ile Lys Gly Gly Leu Phe Ala Asp Ile Ala Ser His Pro
63      275      280      285
64 Trp Gln Ala Ala Ile Phe Ala Lys His Arg Arg Ser Pro Gly Glu Arg
65      290      295      300
66 Phe Leu Cys Gly Gly Ile Leu Ile Ser Ser Cys Trp Ile Leu Ser Ala
67 305      310      315      320
68 Ala His Cys Phe Gln Glu Arg Phe Pro Pro His His Leu Thr Val Ile
69      325      330      335
70 Leu Gly Arg Thr Tyr Arg Val Val Pro Gly Glu Glu Glu Gln Lys Phe
71      340      345      350
72 Glu Val Glu Lys Tyr Ile Val His Lys Glu Phe Asp Asp Thr Tyr
73      355      360      365
74 Asp Asn Asp Ile Ala Leu Leu Gln Leu Lys Ser Asp Ser Ser Arg Cys
75      370      375      380
76 Ala Gln Glu Ser Ser Val Val Arg Thr Val Cys Leu Pro Pro Ala Asp
77 385      390      395      400
78 Leu Gln Leu Pro Asp Trp Thr Glu Cys Glu Leu Ser Gly Tyr Gly Lys
79      405      410      415
80 Asp Glu Ala Leu Ser Pro Phe Tyr Ser Glu Arg Leu Lys Glu Ala His
81      420      425      430
82 Val Arg Leu Tyr Pro Ser Ser Arg Cys Thr Ser Gln His Leu Leu Asn
83      435      440      445
84 Arg Thr Val Thr Asp Asn Met Leu Cys Ala Gly Asp Thr Arg Ser Gly
85      450      455      460
86 Gly Pro Gln Ala Asn Leu His Asp Ala Cys Gln Gly Asp Ser Gly Gly
87 465      470      475      480
88 Pro Leu Val Cys Leu Asn Asp Gly Arg Met Thr Leu Val Gly Ile Ile
89      485      490      495
90 Ser Trp Gly Leu Gly Cys Gly Gln Lys Asp Val Pro Gly Val Tyr Thr
91      500      505      510
92 Lys Val Thr Asn Tyr Leu Asp Trp Ile Arg Asp Asn Met Arg Pro
93      515      520      525
96 <210> SEQ ID NO: 2
97 <211> LENGTH: 527
98 <212> TYPE: PRT
99 <213> ORGANISM: Homo sapiens
101 <400> SEQUENCE: 2
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103 1      5      10      15
104 Gln His Gln Ser Trp Leu Arg Pro Val Leu Arg Ser Asn Arg Val Glu
105      20      25      30
106 Tyr Cys Trp Cys Asn Ser Gly Arg Ala Gln Cys His Ser Val Pro Val

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107          35          40          45
108 Lys Ser Cys Ser Glu Pro Arg Cys Phe Asn Gly Gly Thr Cys Gln Gln
109          50          55          60
110 Ala Leu Tyr Phe Ser Asp Phe Val Cys Gln Cys Pro Glu Gly Phe Ala
111 65          70          75          80
112 Gly Lys Cys Cys Glu Ile Asp Thr Arg Ala Thr Cys Tyr Glu Asp Gln
113          85          90          95
114 Gly Ile Ser Tyr Arg Gly Thr Trp Ser Thr Ala Glu Ser Gly Ala Glu
115          100          105          110
116 Cys Thr Asn Trp Asn Ser Ser Ala Leu Ala Gln Lys Pro Tyr Ser Gly
117          115          120          125
118 Arg Arg Pro Asp Ala Ile Arg Leu Gly Leu Gly Asn His Asn Tyr Cys
119          130          135          140
120 Arg Asn Pro Asp Arg Asp Ser Lys Pro Trp Cys Tyr Val Phe Lys Ala
121 145          150          155          160
122 Gly Lys Tyr Ser Ser Glu Phe Cys Ser Thr Pro Ala Cys Ser Glu Gly
123          165          170          175
124 Asn Ser Asp Cys Tyr Phe Gly Asn Gly Ser Ala Tyr Arg Gly Thr His
125          180          185          190
126 Ser Leu Thr Glu Ser Gly Ala Ser Cys Leu Pro Trp Asn Ser Met Ile
127          195          200          205
128 Leu Ile Gly Lys Val Tyr Thr Ala Gln Asn Pro Ser Ala Gln Ala Leu
129          210          215          220
130 Gly Leu Gly Lys His Asn Tyr Cys Arg Asn Pro Asp Gly Asp Ala Lys
131 225          230          235          240
132 Pro Trp Cys His Val Leu Lys Asn Arg Arg Leu Thr Trp Glu Tyr Cys
133          245          250          255
134 Asp Val Pro Ser Cys Ser Thr Cys Gly Leu Arg Gln Tyr Ser Gln Pro
135          260          265          270
136 Gln Phe Glu Ile Lys Gly Gly Leu Phe Ala Asp Ile Ala Ser His Pro
137          275          280          285
138 Trp Gln Ala Ala Ile Phe Ala Lys His Arg Arg Ser Pro Gly Glu Arg
139          290          295          300
140 Phe Leu Cys Gly Gly Ile Leu Ile Ser Ser Cys Trp Ile Leu Ser Ala
141 305          310          315          320
142 Ala His Cys Phe Gln Glu Arg Phe Pro Pro His His Leu Thr Val Ile
143          325          330          335
144 Leu Gly Arg Thr Tyr Arg Val Val Pro Gly Glu Glu Glu Gln Lys Phe
145          340          345          350
146 Glu Val Glu Lys Tyr Ile Val His Lys Glu Phe Asp Asp Asp Thr Tyr
147          355          360          365
148 Asp Asn Asp Ile Ala Leu Leu Gln Leu Lys Ser Asp Ser Ser Arg Cys
149          370          375          380
150 Ala Gln Glu Ser Ser Val Val Arg Thr Val Cys Leu Pro Pro Ala Asp
151 385          390          395          400
152 Leu Gln Leu Pro Asp Trp Thr Glu Cys Glu Leu Ser Gly Tyr Gly Lys
153          405          410          415
154 Glu Glu Ala Leu Ser Pro Phe Tyr Ser Glu Arg Leu Lys Glu Ala His
155          420          425          430

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156 Val Arg Leu Tyr Pro Ser Ser Arg Cys Thr Ser Gln His Leu Leu Asn
157      435      440      445
158 Arg Thr Val Thr Asp Asn Met Leu Cys Ala Gly Asp Thr Arg Ser Gly
159      450      455      460
160 Gly Pro Gln Ala Asn Leu His Asp Ala Cys Gln Gly Asp Ser Gly Gly
161 465      470      475      480
162 Pro Leu Val Cys Leu Asn Asp Gly Arg Met Thr Leu Val Gly Ile Ile
163      485      490      495
164 Ser Trp Gly Leu Gly Cys Gly Gln Lys Asp Val Pro Gly Val Tyr Thr
165      500      505      510
166 Lys Val Thr Asn Tyr Leu Asp Trp Ile Arg Asp Asn Met Arg Pro
167      515      520      525
170 <210> SEQ ID NO: 3
171 <211> LENGTH: 527
172 <212> TYPE: PRT
173 <213> ORGANISM: Homo sapiens
175 <400> SEQUENCE: 3
176 Ser Tyr Gln Val Ile Cys Arg Asp Glu Lys Thr Gln Met Ile Tyr Gln
177 1      5      10      15
178 Gln His Gln Ser Trp Leu Arg Pro Val Leu Arg Ser Asn Arg Val Glu
179      20      25      30
180 Tyr Cys Trp Cys Asn Ser Gly Arg Ala Gln Cys His Ser Val Pro Val
181      35      40      45
182 Lys Ser Cys Ser Glu Pro Arg Cys Phe Asn Gly Gly Thr Cys Gln Gln
183      50      55      60
184 Ala Leu Tyr Phe Ser Asp Phe Val Cys Gln Cys Pro Glu Gly Phe Ala
185 65      70      75      80
186 Gly Lys Cys Cys Glu Ile Asp Thr Arg Ala Thr Cys Tyr Glu Asp Gln
187      85      90      95
188 Gly Ile Ser Tyr Arg Gly Thr Trp Ser Thr Ala Glu Ser Gly Ala Glu
189      100      105      110
190 Cys Thr Asn Trp Asn Ser Ser Ala Leu Ala Gln Lys Pro Tyr Ser Gly
191      115      120      125
192 Arg Arg Pro Asp Ala Ile Arg Leu Gly Leu Gly Asn His Asn Tyr Cys
193      130      135      140
194 Arg Asn Pro Asp Arg Asp Ser Lys Pro Trp Cys Tyr Val Phe Lys Ala
195 145      150      155      160
196 Gly Lys Tyr Ser Ser Glu Phe Cys Ser Thr Pro Ala Cys Ser Glu Gly
197      165      170      175
198 Asn Ser Asp Cys Tyr Phe Gly Asn Gly Ser Ala Tyr Arg Gly Thr His
199      180      185      190
200 Ser Leu Thr Glu Ser Gly Ala Ser Cys Leu Pro Trp Asn Ser Met Ile
201      195      200      205
202 Leu Ile Gly Lys Val Tyr Thr Ala Gln Asn Pro Ser Ala Gln Ala Leu
203      210      215      220
204 Gly Leu Gly Lys His Asn Tyr Cys Arg Asn Pro Asp Gly Asp Ala Lys
205 225      230      235      240
206 Pro Trp Cys His Val Leu Lys Asn Arg Arg Leu Thr Trp Glu Tyr Cys
207      245      250      255

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```

208 Asp Val Pro Ser Cys Ser Thr Cys Gly Leu Arg Gln Tyr Ser Gln Pro
209                260                265                270
210 Gln Phe Glu Ile Lys Gly Gly Leu Phe Ala Asp Ile Ala Ser His Pro
211                275                280                285
212 Trp Gln Ala Ala Ile Phe Ala Lys His Arg Arg Ser Pro Gly Glu Arg
213                290                295                300
214 Phe Leu Cys Gly Gly Ile Leu Ile Ser Ser Cys Trp Ile Leu Ser Ala
215 305                310                315                320
216 Ala His Cys Phe Gln Glu Arg Phe Pro Pro His His Leu Thr Val Ile
217                325                330                335
218 Leu Gly Arg Thr Tyr Arg Val Val Pro Gly Glu Glu Glu Gln Lys Phe
219                340                345                350
220 Glu Val Glu Lys Tyr Ile Val His Lys Glu Phe Asp Asp Asp Thr Tyr
221                355                360                365
222 Asp Asn Asp Ile Ala Leu Leu Gln Leu Lys Ser Asp Ser Ser Arg Cys
223                370                375                380
224 Ala Gln Glu Ser Ser Val Val Arg Thr Val Cys Leu Pro Pro Ala Asp
225 385                390                395                400
226 Leu Gln Leu Pro Asp Trp Thr Glu Cys Glu Leu Ser Gly Tyr Gly Lys
227                405                410                415
228 His Glu Ala Leu Ser Pro Phe Tyr Ser Glu Arg Leu Tyr Glu Ala His
229                420                425                430
230 Val Arg Leu Tyr Pro Ser Ser Arg Cys Thr Ser Gln His Leu Leu Asn
231                435                440                445
232 Arg Thr Val Thr Asp Asn Met Leu Cys Ala Gly Asp Thr Arg Ser Gly
233                450                455                460
234 Gly Pro Gln Ala Asn Leu His Asp Ala Cys Gln Gly Asp Ser Gly Gly
235 465                470                475                480
236 Pro Leu Val Cys Leu Asn Asp Gly Arg Met Thr Leu Val Gly Ile Ile
237                485                490                495
238 Ser Trp Gly Leu Gly Cys Gly Gln Lys Asp Val Pro Gly Val Tyr Thr
239                500                505                510
240 Lys Val Thr Asn Tyr Leu Asp Trp Ile Arg Asp Asn Met Arg Pro
241                515                520                525
244 <210> SEQ ID NO: 4
245 <211> LENGTH: 290
246 <212> TYPE: DNA
247 <213> ORGANISM: Homo sapiens
249 <400> SEQUENCE: 4
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252 caacatgctg tgtgctggag aactcggag cggcggggccc caggcaaact tgcacgacgc 180
253 ctgccagggc gattcgggag gccccctggt gtgtctgaac gatggccgca tgactttggt 240
254 gggcatcatc agctggggcc tgggctgtgg acagaaggat gtcccgggtg 290
256 <210> SEQ ID NO: 5
257 <211> LENGTH: 290
258 <212> TYPE: DNA
259 <213> ORGANISM: Homo sapiens
261 <400> SEQUENCE: 5

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VERIFICATION SUMMARY

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